

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/509,073 B
Source: IFWP
Date Processed by STIC: 06/29/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 06/29/2006

PATENT APPLICATION: US/10/509,073B

TIME: 10:15:42

Input Set : A:\TSUNEOKA Seq. Listing revised and filed 2006-02-03.txt

Output Set: N:\CRF4\06292006\J509073B.raw

4 <110> APPLICANT: TSUNEOKA, Makoto
 5 KIMURA, Hiroshi
 7 <120> TITLE OF INVENTION: Cancer-Associated Gene Mina53, Protein Mina53
 8 and Monoclonal Antibody Thereof
 10 <130> FILE REFERENCE: 2004-1597A/WMC/00279
 12 <140> CURRENT APPLICATION NUMBER: 10/509,073B
 C--> 13 <141> CURRENT FILING DATE: 2004-10-12
 15 <160> NUMBER OF SEQ ID NOS: 3
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1395
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
 22 <400> SEQUENCE: 1

23	atg cca aag aaa gca aag cct aca ggg agt ggg aag gaa gag ggg ccg	48
24	Met Pro Lys Lys Ala Lys Pro Thr Gly Ser Gly Lys Glu Glu Gly Pro	
25	5 10 15	
27	gct ccc tgt aag cag atg aag tta gaa gca gct ggg ggg cct tca gct	96
28	Ala Pro Cys Lys Gln Met Lys leu Glu Ala Ala Gly Gly Pro Ser Ala	
29	20 25 30	
31	tta aac ttt gac agt ccc agt agt ctc ttt gaa agt tta atc tcg ccc	144
32	Leu Asn Phe Asp Ser Pro Ser Ser Leu Phe Glu Ser Leu Ile Ser Pro	
33	35 40 45	
35	atc aag aca gag act ttt ttc aag gaa ttc tgg gag cag aag ccc ctt	192
36	Ile Lys Thr Glu Thr Phe Phe Lys Glu Phe Trp Glu Gln Lys Pro Leu	
37	50 55 60	
39	ctc att cag aga gat gac cct gca ctg gcc aca tac tat ggg tcc ctg	240
40	Leu Ile Gln Arg Asp Asp Pro Ala Leu Ala Thr Tyr Tyr Gly Ser Leu	
41	65 70 75 80	
43	ttc aag cta aca gat ctg aag agt ctg tgc agc cgg ggg atg tac tat	288
44	Phe Lys Leu Thr Asp Leu Lys Ser Leu Cys Ser Arg Gly Met Tyr Tyr	
45	85 90 95	
47	gga aga gat gtg aat gtc tgc cgg tgt gtc aat ggg aag aag aag gtt	336
48	Gly Arg Asp Val Asn Val Cys Arg Cys Val Asn Gly Lys Lys Lys Val	
49	100 105 110	
51	tta aat aaa gat ggc aaa gca cac ttt ctt cag ctg aga aaa gat ttt	384
52	Leu Asn Lys Asp Gly Lys Ala His Phe Leu Gln Leu Arg Lys Asp Phe	
53	115 120 125	
55	gat cag aaa agg gca acg att cag ttt cac caa cct cag aga ttt aag	432
56	Asp Gln Lys Arg Ala Thr Ile Gln Phe His Gln Pro Gln Arg Phe Lys	
57	130 135 140	
59	gat gag ctt tgg agg atc cag gag aag ctg gaa tgt tac ttt ggc tcc	480
60	Asp Glu Leu Trp Arg Ile Gln Glu Lys Leu Glu Cys Tyr Phe Gly Ser	
61	145 150 155 160	

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63	ttg gtt ggc tgc aat gtg tac ata act ccc gca gga tct cag ggc ctg	528
64	Leu Val Gly Ser Asn Val Tyr Ile Thr Pro Ala Gly Ser Gln Gly Leu	
65	165 170 175	
67	ccg ccc cat tat gat gat gtc gag gtt ttc atc ctg cag ctg gag gga	576
68	Pro Pro His Tyr Asp Asp Val Glu Val Phe Ile Leu Gln Leu Glu Gly	
69	180 185 190	
71	gag aaa cac tgg cgc ctc tac cac ccc act gtg ccc ctg gca cga gag	624
72	Glu Lys His Trp Arg Leu Tyr His Pro Thr Val Pro Leu Ala Arg Glu	
73	195 200 205	
75	tac agc gtg gag gcc gag gaa agg atc ggc agg ccg gtg cat gag ttt	672
76	Tyr Ser Val Glu Ala Glu Glu Arg Ile Gly Arg Pro Val His Glu Phe	
77	210 215 220	
79	atg ctg aag ccg ggt gat ttg ttg tac ttt ccc aga gga acc att cat	720
80	Met Leu Lys Pro Gly Asp Leu Leu Tyr Phe Pro Arg Gly Thr Ile His	
81	225 230 235 240	
83	caa gcg gac act cct gcg ggg ctg gcc cac tcg act cac gtg acc atc	768
84	Glu Ala Asp Thr Pro Ala Gly Leu Ala His Ser Thr His Val Thr Ile	
85	245 250 255	
87	agc acc tac cag aac aat tca tgg gga gat ttc ctt ttg gat acc atc	816
88	Ser Thr Tyr Gln Asn Asn Ser Trp Gly Asp Phe Leu Leu Asp Thr Ile	
89	260 265 270	
91	tcg ggg ctt gta ttt gat act gca aag gaa gac gtg gag tta cgg acc	864
92	Ser Gly Leu Val Phe Asp Thr Ala Lys Glu Asp Val Glu Leu Arg Thr	
93	275 280 285	
95	ggc ata ccc cgg cag ctg ctc ctg gtg gaa tcc aca act gtt gct aca	912
96	Gly Ile Pro Arg Gln Leu Leu Leu Val Glu Ser Thr Thr Val Ala Thr	
97	290 295 300	
99	aga cga tta agt ggc ttc ctg agg aca ctt gca gac cgg ctg gag ggc	960
100	Arg Arg Leu Ser Gly Phe Leu Arg Thr Leu Ala Asp Arg Leu Glu Gly	
101	305 310 315 320	
103	acc aaa gaa ctg ctt tcc tca gac atg aag gat ttt att atg cac	1008
104	Thr Lys Glu Leu Leu Ser Ser Asp Met Lys Lys Asp Phe Ile Met His	
105	325 330 335	
107	aga ctc ccc cct tac tct gcg gga gat ggg gca gag ctg tca aca cca	1056
108	Arg Leu Pro Pro Tyr Ser Ala Gly Asp Gly Ala Glu Leu Ser Thr Pro	
109	340 345 350	
111	ggt gga aag tta ccg agg ctg gac agt gta gtg aga ctg cag ttt aaa	1104
112	Gly Gly Lys Leu Pro Arg Leu Asp Ser Val Val Arg Leu gln Phe Lys	
113	355 360 365	
115	gac cac att gtc ctc aca gta ctg ccg gat caa gat caa tct gat gaa	1152
116	Asp His Ile Val Leu Thr Val Leu Pro Asp Gln Asp Gln Ser Asp Glu	
117	370 375 380	
119	gct caa gaa aag atg gtg tac atc tat cat tcc tta aag aat agt aga	1200
120	Ala Gln Glu Lys Met Val Tyr Ile Tyr His Ser Leu Lys Asn Ser Arg	
121	385 390 395 400	
123	gag aca cac atg atg gga aat gag gag gaa aca gag ttt cat gga ctt	1248
124	Glu Thr His Met Met Gly Asn Glu Glu Glu Thr Glu Phe His Gly Leu	
125	405 410 415	
127	cgc ttc cct ttg tca cat ttg gat gca ctg aag caa att tgg aat agt	1296

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128 Arg Phe Pro Leu Ser His Leu Asp Ala Leu Lys Gln Ile Trp Asn Ser
129          420          425          430
131 cca gct att tct gtc aag gac ctg aaa ctt act aca gat gag gaa aag 1344
132 Pro Ala Ile Ser Val Lys Asp Leu Lys Leu Thr Thr Asp Glu Glu Lys
133          435          440          445
135 gaa agc ctg gta tta tcc ctc tgg aca gaa tgt tta att caa gta gtc 1392
136 Glu Ser Leu Val Leu Ser Leu Trp Thr Glu Cys Leu Ile Gln Val Val
137          450          455          460
139 tag 1395
142 <210> SEQ ID NO: 2
143 <211> LENGTH: 1398
144 <212> TYPE: DNA
145 <213> ORGANISM: Mus musculus
147 <400> SEQUENCE: 2
148 atg cca aag aaa gtg cag ccc aca ggg gat gag aac gaa gaa gag tct 48
149 Met Pro Lys Lys Val Gln Pro Thr Gly Asp Glu Asn Glu Glu Glu Ser
150          5          10          15
152 gtt cct tgc aag cgg gtg aag gag gag ctg cct gaa acg ctt tct gta 96
153 Val Pro Cys Lys Arg Val Lys Glu Glu Leu Pro Glu Thr Leu Ser Val
154          20          25          30
156 tta aac ttt gac agc ccc agt agt ttc ttc gaa agt tta atc tca ccc 144
157 Leu Asn Phe Asp Ser Pro Ser Ser Phe Phe Glu Ser Leu Ile Ser Pro
158          35          40          45
160 atc aaa gta gag act ttt ttc aag gaa ttc tgg gaa caa aag ccc ctt 192
161 Ile Lys Val Glu Thr Phe Phe Lys Glu Phe Trp Glu Gln Lys Pro Leu
162          50          55          60
164 ctc att cag agg gat gac cct gta ctg gcc aaa tat tac cag tct ctg 240
165 Leu Ile Gln Arg Asp Asp Pro Val Leu Ala Lys Tyr Tyr Gln Ser Leu
166          65          70          75          80
168 ttc agc ctc tca gat ctg aag aga ctc tgc aag aaa gga gtg tac tat 288
169 Phe Ser Leu Ser Asp Leu Lys Arg Leu Cys Lys Lys Gly Val Tyr Tyr
170          85          90          95
172 gga aga gac gtg aat gtc tgc cgg agc atc agt ggg aag aag aag gtt 336
173 Gly Arg Asp Val Asn Val Cys Arg Ser Ile Ser Gly Lys Lys Lys Val
174          100          105          110
176 tta aat aag gat ggc aga gca cat ttt ctt cag ctg aga aaa gat ttt 384
177 Leu Asn Lys Asp Gly Arg Ala His Phe Leu Gln Leu Arg Lys Asp Phe
178          115          120          125
180 gat cag aag agg gca aca att cag ttt cac caa cct cag aga tat aag 432
181 Asp Gln Lys Arg Ala Thr Ile Gln Phe His Gln Pro Gln Arg Tyr Lys
182          130          135          140
184 gat gag ctg tgg cgg atc cag gaa aag ctg gaa tgt tac ttt ggg tcc 480
185 Asp Glu Leu Trp Arg Ile Gln Glu Lys Leu Glu Cys Tyr Phe Gly Ser
186          145          150          155          160
188 tta gta ggc tcg aat gtg tac atg act cct gca gga tct cag ggc ctc 528
189 Leu Val Gly Ser Asn Val Tyr Met Thr Pro Ala Gly Ser Gln Gly Leu
190          165          170          175
192 cct cca cat tat gat gtt gag gtt ttt atc ctg cag ctg gag gga 576
193 Pro Pro His Tyr Asp Asp Val Glu Val Phe Ile Leu Gln Leu Glu Gly

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194	180	185	190	
196	acg aaa cac tgg cgc ctg tac tcc cca act gtg ccc ctg gca cac gag	624		
197	Thr Lys His Trp Arg Leu Tyr Ser Pro Thr Val Pro Leu Ala His Glu			
198	195 200 205			
200	tac agt gtg gaa tct gag gac cgg atc ggc aca ccg aca cac gac ttc	672		
201	Tyr Ser Val Glu Ser Glu Asp Arg Ile Gly Thr Pro Thr His Asp Phe			
202	210 215 220			
204	ctg ctg aag cct gga gat ttg ttg tac ttt ccc aga ggg acc att cat	720		
205	Leu Leu Lys Pro Gly Asp Leu Leu Tyr Phe Pro Arg Gly Thr Ile His			
206	225 230 235 240			
208	cag gca gaa act cct tca ggc ctg gcc tac tct att cac ctg act att	768		
209	Gln Ala Glu Thr Pro Ser Gly Leu Ala Tyr Ser Ile His Leu Thr Ile			
210	245 250 255			
212	agc acc tac cag aac aat tca tgg gga gac tgc ctt ttg gat tcc att	816		
213	Ser Thr Tyr Gln Asn Asn Ser Trp Gly Asp Cys Leu Leu Asp Ser Ile			
214	260 265 270			
216	tgc ggg ttc gta ttt gac att gca aag gaa gat gtg gca tta agg agt	864		
217	Ser Gly Phe Val Phe Asp Ile Ala Lys Glu Asp Val Ala Leu Arg Ser			
218	275 280 285			
220	gga atg ccc cgg cgg atg ctc ctg aat gtg gaa acc cca gct gat gta	912		
221	Gly Met Pro Arg Arg Met Leu Leu Asn Val Glu Thr Pro Ala Asp Val			
222	290 295 300			
224	aca agg aag ttg agt ggc ttt ctg agg act ctt gca gac cag ctc gag	960		
225	Thr Arg Lys Leu Ser Gly Phe Leu Arg Thr Leu Ala Asp Gln Leu Glu			
226	305 310 315 320			
228	ggc aga gaa gag ctg ctg tca tca gat atg aag aag gac ttc gtc aag	1008		
229	Gly Arg Glu Glu Leu Leu Ser Ser Asp Met Lys Lys Asp Phe Val Lys			
230	325 330 335			
232	cac aga ctc cct cct ttc ttc gag gga aat gga acg gag acg atg gac	1056		
233	His Arg Leu Pro Phe Phe Glu Gly Asn Gly Thr Glu Thr Met Asp			
234	340 345 350			
236	cca ggt aaa cag ttg cca agg ttg gac aac ata ata aga ctg cag ttc	1104		
237	Pro Gly Lys Gln Leu Pro Arg Leu Asp Asn Ile Ile Arg Leu Gln Phe			
238	355 360 365			
240	aaa gat cac att gtc ctc aca gta ggg cca gat aag aat cca ttt gat	1152		
241	Lys Asp His Ile Val Leu Thr Val Gly Pro Asp Lys Asn Pro Phe Asp			
242	370 375 380			
244	gaa gct caa caa aag gtg gtt tac atc tat cat tct ctg aag aat gtg	1200		
245	Glu Ala Gln Gln Lys Val Val Tyr Ile Tyr His Ser Leu Lys Asn Val			
246	385 390 395 400			
248	agg cag atg cac atg ata gga gaa gag gag gaa tcc gag att ttc ggt	1248		
249	Arg Gln Met His Met Ile Gly Glu Glu Glu Glu Ser Glu Ile Phe Gly			
250	405 410 415			
252	ctt cgc ttt cct tta tca cat gtg gat gct ctg aag caa atc tgg tgc	1296		
253	Leu Arg Phe Pro Leu Ser His Val Asp Ala Leu Lys Gln Ile Trp Cys			
254	420 425 430			
256	ggg tca cca att cgt gtt aag gaa ctg aaa ctt gac aca gat gaa gaa	1344		
257	Gly Ser Pro Ile Arg Val Lys Glu Leu Lys Leu Asp Thr Asp Glu Glu			
258	435 440 445			

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260 aag gag aac ctg gca ctg tct ctc tgg tcg gag tct tta atc caa gta      1392
261 Lys Glu Asn Leu Ala Leu Ser Leu Trp Ser Glu Ser Leu Ile Gln Val
262      450                      455                      460
263 ctc tag                                                                1398
264 Leu
265 465
268 <210> SEQ ID NO: 3
269 <211> LENGTH: 1398
270 <212> TYPE: DNA
271 <213> ORGANISM: Rattus norvegicus
273 <400> SEQUENCE: 3
274 atg cca aag aaa gtg aag ccc aca ggg gat gag aat gaa gaa gag tct      48
275 Met Pro Lys Lys Val Lys Pro Thr Gly Asp Glu Asn Glu Glu Glu Ser
276      5                      10                      15
278 gtt cct tgc aag cag gtg aaa gag gag cta cct aat acg ctt tct gta      96
279 Val Pro Cys Lys Gln Val Lys Glu Glu Leu Pro Asn Thr Leu Ser Val
280      20                      25                      30
282 tta aac ttt gac agc ccc agt agt ttc ttt gaa agt tta ata tca ccc      144
283 Leu Asn Phe Asp Ser Pro Ser Ser Phe Phe Glu Ser Leu Ile Ser Pro
284      35                      40                      45
286 atc aaa gta gag aca ttt ttc aag gaa ttc tgg gaa cag aag ccc ctt      192
287 Ile Lys Val Glu Thr Phe Phe Lys Glu Phe Trp Glu Gln Lys Pro Leu
288      50                      55                      60
290 ctc att cag aga gat gac cct tcg ctg gcc gca tat tac cag tct ctg      240
291 Leu Ile Gln Arg Asp Asp Pro Ser Leu Ala Ala Tyr Tyr Gln Ser Leu
292      65                      70                      75                      80
294 ttc agc ctc tca gat ctg agg agt ctc tgc agc caa ggg ctg tac tat      288
295 Phe Ser Leu Ser Asp Leu Arg Ser Leu Cys Ser Gln Gly Leu Tyr Tyr
296      85                      90                      95
298 gga aga gat gtc aat gtc tgc cgg tgc atc ggt ggg aag aag aag gtt      336
299 Gly Arg Asp Val Asn Val Cys Arg Cys Ile Gly Gly Lys Lys Lys Val
300      100                     105                     110
302 tta aat aag gat ggc aaa gca cag ttt ctt cag ctg aga aaa gat ttt      384
303 Leu Asn Lys Asp Gly Lys Ala Gln Phe Leu Gln Leu Arg Lys Asp Phe
304      115                     120                     125
306 gat cag aag agg gca aca att cag ttt cat cag cca cag aga ttt aag      432
307 Asp Gln Lys Arg Ala Thr Ile Gln Phe His Gln Pro Gln Arg Phe Lys
308      130                     135                     140
310 gat gag ctc tgg agg atc cag gaa aag ctg gaa tgt tac ttt ggc tcc      480
311 Asp Glu Leu Trp Arg Ile Gln Glu Lys Leu Glu Cys Tyr Phe Gly Ser
312      145                     150                     155                     160
314 tta gta ggc tca aat gtg tac atg act ccc gca gga tct cag ggc ctt      528
315 Leu Val Gly Ser Asn Val Tyr Met Thr Pro Ala Gly Ser Gln Gly Leu
316      165                     170                     175
318 cct cca cat tac gac gat gtt gag gtt ttt atc ctg cag ctg gag gga      576
319 Pro Pro His Tyr Asp Asp Val Glu Val Phe Ile Leu Gln Leu Glu Gly
320      180                     185                     190
322 agg aaa cgt tgg cgc ctg tac tcc cca act gtg ccc ctg gcg cgt gag      624
323 Arg Lys Arg Trp Arg Leu Tyr Ser Pro Thr Val Pro Leu Ala Arg Glu

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/29/2006
PATENT APPLICATION: US/10/509,073B TIME: 10:15:43

Input Set : A:\TSUNEOKA Seq. Listing revised and filed 2006-02-03.txt
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 170,190

Seq#:3; Line(s) 356

VERIFICATION SUMMARY

DATE: 06/29/2006

PATENT APPLICATION: US/10/509,073B

TIME: 10:15:43

Input Set : A:\TSUNEOKA Seq. Listing revised and filed 2006-02-03.txt

Output Set: N:\CRF4\06292006\J509073B.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date